

SEQUENCE LISTING



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SHIMAUCHI, JUNKO
MATSUMOTO, MARIKO

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CARGO RECEPTORS

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<140> 10/525,020

<141> 2005-02-18

<150> PCT/JP03/01718

<151> 2003-02-18

<150> JP 2002-238559

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<160> 33

<170> PatentIn Ver. 3.3

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<212> DNA

<213> Homo sapiens

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<222> (22)..(1554)

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ttc gtc cgg ggc gac ggc gtg gga gga gac ccc gcg gtc gcg ttg cca	147
Phe Val Arg Gly Asp Gly Val Gly Gly Asp Pro Ala Val Ala Leu Pro	
30 35 40	
cat cgc cgt ttc gag tac aaa tac agc ttc aag ggg ccg cac ctg gtg	195
His Arg Arg Phe Glu Tyr Lys Tyr Ser Phe Lys Gly Pro His Leu Val	
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Gln Ser Asp Gly Thr Val Pro Phe Trp Ala His Ala Gly Asn Ala Ile	
60 65 70	
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Pro Ser Ser Asp Gln Ile Arg Val Ala Pro Ser Leu Lys Ser Gln Arg	
75 80 85 90	

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Gly Ser Val Trp Thr Lys Thr Lys Ala Ala Phe Glu Asn Trp Glu Val	
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gag gtg aca ttt cga gtg act gga aga ggt cga att gga gct gat ggc	387
Glu Val Thr Phe Arg Val Thr Gly Arg Gly Arg Ile Gly Ala Asp Gly	
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cta gca att tgg tat gca gaa aat caa ggc ttg gag ggc cct gtg ttt	435
Leu Ala Ile Trp Tyr Ala Glu Asn Gln Gly Leu Glu Gly Pro Val Phe	
125 130 135	
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Gly Ser Ala Asp Leu Trp Asn Gly Val Gly Ile Phe Phe Asp Thr Phe	
140 145 150	
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Asp Asn Asp Gly Lys Lys Asn Asn Pro Ala Ile Val Ile Ile Gly Asn	
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Asn Gly Gln Ile His Tyr Asp His Gln Asn Asp Gly Ala Ser Gln Ala	
175 180 185	
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Leu Ala Ser Cys Gln Arg Asp Phe Arg Asn Lys Pro Tyr Pro Val Arg	
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Ala Lys Ile Thr Tyr Tyr Gln Asn Thr Leu Thr Val Met Ile Asn Asn	
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Gly Phe Thr Pro Asp Lys Asn Asp Tyr Glu Phe Cys Ala Lys Val Glu	
220 225 230	
aat atg att atc cct gca caa ggg cat ttt gga ata tct gct gca act	771
Asn Met Ile Ile Pro Ala Gln Gly His Phe Gly Ile Ser Ala Ala Thr	
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Gly Gly Leu Ala Asp Asp His Asp Val Leu Ser Phe Leu Thr Phe Gln	
255 260 265	
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Leu Thr Glu Pro Gly Lys Glu Pro Pro Thr Pro Asp Lys Glu Ile Ser	
270 275 280	
gaa aag gaa aaa gaa aag tat cag gag gaa ttt gag cac ttt caa caa	915
Glu Lys Glu Lys Glu Lys Tyr Gln Glu Glu Phe Glu His Phe Gln Gln	
285 290 295	
gaa ttg gat aaa aaa aaa gag gaa ttc cag aag ggc cac ccc gac ctc	963
Glu Leu Asp Lys Lys Lys Glu Glu Phe Gln Lys Gly His Pro Asp Leu	
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cta aga caa gtc ttt gaa gga cag aat cgt att cat ctt gaa atc aag 1059
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 335 340 345

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gtc tct tcc tta aca gag gaa atc tct aaa aga gga gca gga atg cct 1155
 Val Ser Ser Leu Thr Glu Glu Ile Ser Lys Arg Gly Ala Gly Met Pro
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 Gly Gln His Gly Gln Ile Thr Gln Gln Glu Leu Asp Thr Val Val Lys
 380 385 390

act cag cat gag att ctg aga caa gta aat gaa atg aaa aat tcc atg 1251
 Thr Gln His Glu Ile Leu Arg Gln Val Asn Glu Met Lys Asn Ser Met
 395 400 405 410

agt gaa acc gtc aga ctg gtc agt gga atg cag cac cct ggc tct gct 1299
 Ser Glu Thr Val Arg Leu Val Ser Gly Met Gln His Pro Gly Ser Ala
 415 420 425

gga ggc gtc tat gag aca aca cag cac ttc att gac atc aaa gag cac 1347
 Gly Gly Val Tyr Glu Thr Thr Gln His Phe Ile Asp Ile Lys Glu His
 430 435 440

ctg cac ata gta aag agg gac ata gat aac tta gtg cag cga aat atg 1395
 Leu His Ile Val Lys Arg Asp Ile Asp Asn Leu Val Gln Arg Asn Met
 445 450 455

cca tca aat gaa aag ccg aaa tgc cca gaa cta cca cca ttt cca tca 1443
 Pro Ser Asn Glu Lys Pro Lys Cys Pro Glu Leu Pro Pro Phe Pro Ser
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 Cys Leu Ser Thr Val His Phe Ile Ile Phe Val Val Val Gln Thr Val
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 Leu Phe Ile Gly Tyr Ile Met Tyr Arg Ser Gln Gln Glu Ala Ala Ala
 495 500 505

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 Lys Lys Phe Phe
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tgagtcgttt tgagggaatt taagtattta aattgcttca tagtctaaat tattaatttt 1654

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 35 40 45
 Lys Tyr Ser Phe Lys Gly Pro His Leu Val Gln Ser Asp Gly Thr Val
 50 55 60
 Pro Phe Trp Ala His Ala Gly Asn Ala Ile Pro Ser Ser Asp Gln Ile
 65 70 75 80
 Arg Val Ala Pro Ser Leu Lys Ser Gln Arg Gly Ser Val Trp Thr Lys
 85 90 95

Thr Lys Ala Ala Phe Glu Asn Trp Glu Val Glu Val Thr Phe Arg Val
 100 105 110
 Thr Gly Arg Gly Arg Ile Gly Ala Asp Gly Leu Ala Ile Trp Tyr Ala
 115 120 125
 Glu Asn Gln Gly Leu Glu Gly Pro Val Phe Gly Ser Ala Asp Leu Trp
 130 135 140
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 Asn Asn Pro Ala Ile Val Ile Ile Gly Asn Asn Gly Gln Ile His Tyr
 165 170 175
 Asp His Gln Asn Asp Gly Ala Ser Gln Ala Leu Ala Ser Cys Gln Arg
 180 185 190
 Asp Phe Arg Asn Lys Pro Tyr Pro Val Arg Ala Lys Ile Thr Tyr Tyr
 195 200 205
 Gln Asn Thr Leu Thr Val Met Ile Asn Asn Gly Phe Thr Pro Asp Lys
 210 215 220
 Asn Asp Tyr Glu Phe Cys Ala Lys Val Glu Asn Met Ile Ile Pro Ala
 225 230 235 240
 Gln Gly His Phe Gly Ile Ser Ala Ala Thr Gly Gly Leu Ala Asp Asp
 245 250 255
 His Asp Val Leu Ser Phe Leu Thr Phe Gln Leu Thr Glu Pro Gly Lys
 260 265 270
 Glu Pro Pro Thr Pro Asp Lys Glu Ile Ser Glu Lys Glu Lys Glu Lys
 275 280 285
 Tyr Gln Glu Glu Phe Glu His Phe Gln Gln Glu Leu Asp Lys Lys Lys
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 Glu Glu Phe Gln Lys Gly His Pro Asp Leu Gln Gly Gln Pro Ala Glu
 305 310 315 320
 Glu Ile Phe Glu Ser Val Gly Asp Arg Glu Leu Arg Gln Val Phe Glu
 325 330 335
 Gly Gln Asn Arg Ile His Leu Glu Ile Lys Gln Leu Asn Arg Gln Leu
 340 345 350
 Asp Met Ile Leu Asp Glu Gln Arg Arg Tyr Val Ser Ser Leu Thr Glu
 355 360 365
 Glu Ile Ser Lys Arg Gly Ala Gly Met Pro Gly Gln His Gly Gln Ile
 370 375 380
 Thr Gln Gln Glu Leu Asp Thr Val Val Lys Thr Gln His Glu Ile Leu
 385 390 395 400

Arg Gln Val Asn Glu Met Lys Asn Ser Met Ser Glu Thr Val Arg Leu
 405 410 415
 Val Ser Gly Met Gln His Pro Gly Ser Ala Gly Gly Val Tyr Glu Thr
 420 425 430
 Thr Gln His Phe Ile Asp Ile Lys Glu His Leu His Ile Val Lys Arg
 435 440 445
 Asp Ile Asp Asn Leu Val Gln Arg Asn Met Pro Ser Asn Glu Lys Pro
 450 455 460
 Lys Cys Pro Glu Leu Pro Pro Phe Pro Ser Cys Leu Ser Thr Val His
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 Leu Gly Arg Pro Gly Leu Leu Gly Pro Gly Pro Gly Pro Thr Thr Pro
 20 25 30
 ctc ttt ctt ctt ttg ttg ttg ggg tct gtg act gcg gat ata act gac 144
 Leu Phe Leu Leu Leu Leu Leu Gly Ser Val Thr Ala Asp Ile Thr Asp
 35 40 45
 ggc aac agt gaa cat ctc aag cgg gag cat tcg ctc att aag ccc tac 192
 Gly Asn Ser Glu His Leu Lys Arg Glu His Ser Leu Ile Lys Pro Tyr
 50 55 60
 caa ggg gtc ggt tcc agc tct atg ccc ctc tgg gac ttc cag ggc agc 240
 Gln Gly Val Gly Ser Ser Ser Met Pro Leu Trp Asp Phe Gln Gly Ser
 65 70 75 80
 act atg ctc acg agc cag tac gta cgt ctg acc cct gac gag cgc agc 288
 Thr Met Leu Thr Ser Gln Tyr Val Arg Leu Thr Pro Asp Glu Arg Ser
 85 90 95

aaa gag ggc tct atc tgg aac cac cag ccg tgc ttc ctc aaa gac tgg	336
Lys Glu Gly Ser Ile Trp Asn His Gln Pro Cys Phe Leu Lys Asp Trp	
100 105 110	
gaa atg cac gtc cac ttc aaa gtc cac ggc aca ggg aag aag aac ctc	384
Glu Met His Val His Phe Lys Val His Gly Thr Gly Lys Lys Asn Leu	
115 120 125	
cat gga gac ggc atc gcc ttg tgg tac acc cgg gac cgc ctc gtg cca	432
His Gly Asp Gly Ile Ala Leu Trp Tyr Thr Arg Asp Arg Leu Val Pro	
130 135 140	
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Gly Pro Val Phe Gly Ser Lys Asp Asn Phe His Gly Leu Ala Ile Phe	
145 150 155 160	
ctg gac acc tac ccc aat gat gag acc act gag cgc gtg ttc ccg tac	528
Leu Asp Thr Tyr Pro Asn Asp Glu Thr Thr Glu Arg Val Phe Pro Tyr	
165 170 175	
atc tcg gtg atg gtg aac aat ggc tcc ctg tcc tac gac cac agc aag	576
Ile Ser Val Met Val Asn Asn Gly Ser Leu Ser Tyr Asp His Ser Lys	
180 185 190	
gat ggg cgc tgg acc gag ctg gcg ggc tgc acg gct gac ttc cgc aac	624
Asp Gly Arg Trp Thr Glu Leu Ala Gly Cys Thr Ala Asp Phe Arg Asn	
195 200 205	
cgc gat cac gac acc ttc ctg gct gtg cgc tac tcc cgg ggc cgt ctg	672
Arg Asp His Asp Thr Phe Leu Ala Val Arg Tyr Ser Arg Gly Arg Leu	
210 215 220	
acg gtg atg acc gac ctg gag gac aag aac gag tgg aag aac tgc att	720
Thr Val Met Thr Asp Leu Glu Asp Lys Asn Glu Trp Lys Asn Cys Ile	
225 230 235 240	
gac atc acg gga gtg cgc ctg ccc acc ggc tac tac ttc ggg gcc tcc	768
Asp Ile Thr Gly Val Arg Leu Pro Thr Gly Tyr Tyr Phe Gly Ala Ser	
245 250 255	
gcc ggc acc ggc gac ctg tct gac aat cat gac atc atc tcc atg aag	816
Ala Gly Thr Gly Asp Leu Ser Asp Asn His Asp Ile Ile Ser Met Lys	
260 265 270	
ctg ttc cag ctg atg gtg gag cac acg ccc gac gag gag agc atc gac	864
Leu Phe Gln Leu Met Val Glu His Thr Pro Asp Glu Glu Ser Ile Asp	
275 280 285	
tgg acc aag atc gag ccc agc gtc aac ttc ctc aag tcg ccc aaa gac	912
Trp Thr Lys Ile Glu Pro Ser Val Asn Phe Leu Lys Ser Pro Lys Asp	
290 295 300	
aac gtg gac gac ccc acg ggg aac ttc cgc agc ggg ccc ctg acg ggg	960
Asn Val Asp Asp Pro Thr Gly Asn Phe Arg Ser Gly Pro Leu Thr Gly	
305 310 315 320	

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 Trp Arg Val Phe Leu Leu Leu Leu Cys Ala Leu Leu Gly Ile Val Val
 325 330 335

tgc gcc gtg gtg ggg gcc gtg gtg ttc cag aag cgg cag gag cgg aac 1056
 Cys Ala Val Val Gly Ala Val Val Phe Gln Lys Arg Gln Glu Arg Asn
 340 345 350

aag cgc ttc tac tga gtggcgccctc cggcgggggcc tgtccctggg cccaggagcc 1111
 Lys Arg Phe Tyr
 355

aatgtgaact ttttttttta ccgggattat aaaagaacaa caagatgacc ttattttctta 1171

actgtttcaa ataaatgatt aaagtatttt catacatttt gcttcttgcc cagcagggac 1231

aggtggcaga gccgaggctt agggctctggc accccccaca gctggagacg gaggctctcc 1291

tggggctggg gtctcaggag caggggtctg tgtctacaga tgggctgtgg cccctgcagg 1351

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<212> PRT

<213> Homo sapiens

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 35 40 45

Gly Asn Ser Glu His Leu Lys Arg Glu His Ser Leu Ile Lys Pro Tyr
 50 55 60

Gln Gly Val Gly Ser Ser Ser Met Pro Leu Trp Asp Phe Gln Gly Ser
 65 70 75 80

Thr Met Leu Thr Ser Gln Tyr Val Arg Leu Thr Pro Asp Glu Arg Ser
 85 90 95

Lys Glu Gly Ser Ile Trp Asn His Gln Pro Cys Phe Leu Lys Asp Trp
 100 105 110

Glu Met His Val His Phe Lys Val His Gly Thr Gly Lys Lys Asn Leu
 115 120 125

His Gly Asp Gly Ile Ala Leu Trp Tyr Thr Arg Asp Arg Leu Val Pro
 130 135 140

Gly Pro Val Phe Gly Ser Lys Asp Asn Phe His Gly Leu Ala Ile Phe
 145 150 155 160

Leu Asp Thr Tyr Pro Asn Asp Glu Thr Thr Glu Arg Val Phe Pro Tyr
 165 170 175
 Ile Ser Val Met Val Asn Asn Gly Ser Leu Ser Tyr Asp His Ser Lys
 180 185 190
 Asp Gly Arg Trp Thr Glu Leu Ala Gly Cys Thr Ala Asp Phe Arg Asn
 195 200 205
 Arg Asp His Asp Thr Phe Leu Ala Val Arg Tyr Ser Arg Gly Arg Leu
 210 215 220
 Thr Val Met Thr Asp Leu Glu Asp Lys Asn Glu Trp Lys Asn Cys Ile
 225 230 235 240
 Asp Ile Thr Gly Val Arg Leu Pro Thr Gly Tyr Tyr Phe Gly Ala Ser
 245 250 255
 Ala Gly Thr Gly Asp Leu Ser Asp Asn His Asp Ile Ile Ser Met Lys
 260 265 270
 Leu Phe Gln Leu Met Val Glu His Thr Pro Asp Glu Glu Ser Ile Asp
 275 280 285
 Trp Thr Lys Ile Glu Pro Ser Val Asn Phe Leu Lys Ser Pro Lys Asp
 290 295 300
 Asn Val Asp Asp Pro Thr Gly Asn Phe Arg Ser Gly Pro Leu Thr Gly
 305 310 315 320
 Trp Arg Val Phe Leu Leu Leu Leu Cys Ala Leu Leu Gly Ile Val Val
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